

1/31

	130	140	150	160	
1093	GGGGAAACCCAGCACGAGT	GATGTCGTG	CTACCCGCATCT		M.tuberculosis
422	GGGGAAACCCAGCACGAGT	GATGTCGTG	CTACCCGCATCT		M.avium
422	GGGGAAACCCAGCACGAGT	GATGTCGTG	CTACCCGCATCT		M.paratuberc.
507	GGGGAAACCCAGCACGAGT	GATGTCGTG	CTACCCGCATCT		M.phlei
432	GGGGAAACCCAGCACGAGT	GATGTCGTG	CTACCCGCATCT		M.leprae
207	GGGGAAACCCAGCACGAGT	GATGTCGTG	CTACCCGCATCT		M.gastri
150	GGGGAAACCCAGCACGAGT	GATGTCGTG	CTACCCGCATCT		M.kansasii
2588	GGGGAAACCCAGCACGAGT	GATGTCGTG	CTACCCGCATCT		M.smegmatis

	210	220	230	240	
1172	CATCTCAGTACCCGTAGG	AGAGAAAACAATTGTGATTCC			M.tuberculosis
501	CATCTCAGTACCCGTAGG	AGAGAAAACAATTGTGATTCC			M.avium
501	CATCTCAGTACCCGTAGG	AGAGAAAACAATTGTGATTCC			M.paratuberc.
586	CATCTCAGTACCCGTAGG	AGAGAAAACAATTGTGATTCC			M.phlei
511	CATCTCAGTACCCGTAGG	AGAGAAAACAATTGTGATTCC			M.leprae
286	CATCTCAGTACCCGTAGG	AGAGAAAACAATTGTGATTCC			M.gastri
229	CATCTCAGTACCCGTAGG	AGAGAAAACAATTGTGATTCC			M.kansasii
2667	CATCTCAGTACCCGTAGG	AGAGAAAACAATTGTGATTCC			M.smegmatis

	330	340	350	360	
1289	TGTGGGAG-GATATGTCTCAGCGCTACCCGGCTGAGA-GG				M.tuberculosis
617	TGTGGGATTGATATGTCTCAGCTCTACCTGGCTGAGG-GG				M.avium
617	TGTGGGATTGATATGTCTCAGCTCTACCTGGCTGAGG-GG				M.paratuberc.
703	TGTGGGECCTGTGTGTC-CATCGTCCGCCGGCGATGGCAG				M.phlei
629	TGTGGGATTGGTATGTCTCAACTCTACCTGGTTGAGG-GG				M.leprae
404	TGTGGGATCGATAAGTCTCAGCTCTACCCGGCTGAGG-GG				M.gastri
347	TGTGGGATCGATAAGTCTCAGCTCTACCCGGCTGAGG-GG				M.kansasii
2785	TGTGGGACCTATCTTTC-CGCTCTACCTGGCTG-GAGGG				M.smegmatis

Figure 1A

0894377 100399

2/31

	370	380	390	400	
1327	CAGTCAGAAAGTGTCTGGTTAGCGGAAGTGGCCTGGGAT				M.tuberculosis
656	TAGTCAGAAAGTGTCTGGTTAGCGGAAGTGGCCTGGGAT				M.avium
656	TAGTCAGAAAGTGTCTGGTTAGCGGAAGTGGCCTGGGAT				M.paratuberc.
742	TAGTCAGAAAGTGTCTGGTTAGCGGAAGTGGCCTGGGAT				M.phlei
668	TAGTCAGAAAGTGTCTGGTTAGCGGAAGTGGCCTGGGAT				M.leprae
443	CAGTCAGAAAGTGTCTGGTTAGCGGAAGTGGCCTGGGAT				M.gastri
386	CAGTCAGAAAGTGTCTGGTTAGCGGAAGTGGCCTGGGAT				M.kansasii
2823	CAGTCAGAAAGTGTCTGGTTAGCGGAAGTGGCCTGGGAT				M.smegmatis

	450	460	470	480	
1406	CGGCACCTGCCTAGTATCAATTCCCGAGTAGCAGCGGGCC				M.tuberculosis
735	CGGCACCTGCCTATATCAACACCCGAGTAGCAGCGGGCC				M.avium
735	CGGCACCTGCCTATATCAACACCCGAGTAGCAGCGGGCC				M.paratuberc.
820	TGCTGCCGCTGTCACAGG--TCCCGAGTAGCAGCGGGCC				M.phlei
747	TGGCACCTGCCTTGTATCAATTCCCGAGTAGCAGCGGGCC				M.leprae
522	CGGCACCTGCCTTGTATCAATTCCCGAGTAGCAGCGGGCC				M.gastri
465	CGGCACCTGCCTTGTATCAATTCCCGAGTAGCAGCGGGCC				M.kansasii
2902	CGACCTCTGCTTGTATGGTGTTCCTCCGAGTAGCAGCGGGCC				M.smegmatis

	490	500	510	520	
1446	CGTGGGAATCGCTGTGAATCCGCCGGGACCACCCGGTAAG				M.tuberculosis
775	CGTGGGAATCTGCTGTGAATCTGCCGGGACCACCCGGTAAG				M.avium
775	CGTGGGAATCTGCTGTGAATCTGCCGGGACCACCCGGTAAG				M.paratuberc.
857	CGTGGGAATCTGCTGTGAATCTGCCGGGACCACCCGGTAAG				M.phlei
787	CGTGGGAATCTGCTGTGAATCTGCCGGGACCACCCGGTAAG				M.leprae
562	CGTGGGAATCTGCTGTGAATCTGCCGGGACCACCCGGTAAG				M.gastri
505	CGTGGGAATCTGCTGTGAATCTGCCGGGACCACCCGGTAAG				M.kansasii
2942	CGTGGGAATCTGCTGTGAATCTGCCGGGACCACCCGGTAAG				M.smegmatis

Figure 1B

000137 10000

610 620 630 640

1566 GTACCTGAAACCGTGTGCCTACAATCCGTCAGAGCCTCCT M.tuberculosis
 894 GTACCTGAAACCGTGTGCCTACAATCCGTCAGAGCCTCCT M.avium
 894 GTACCTGAAACCGTGTGCCTACAATCCGTCAGAGCCTCCT M.paratuberc.
 976 GTACCTGAAACCGTGTGCCTACAATCCGTCAGAGCCTCCT M.phlei
 907 GTACCTGAAACCGTGTGCCTACAATCCGTCAGAGCCTCCT M.leprae
 682 GTACCTGAAACCGTGTGCCTACAATCCGTCAGAGCCTCCT M.gastri
 625 GTACCTGAAACCGTGTGCCTACAATCCGTCAGAGCCTCCT M.kansasii
 3062 GTACCTGAAACCGTGTGCCTACAATCCGTCAGAGCCTCCT M.smegmatis

650 660 670 680

1606 TTTCTCTCCGAGGAGGGTGGTGATGGCGTGCCTTTTGA M.tuberculosis
 934 C-----GTGGGGTGATGGCGTGCCTTTTGA M.avium
 934 C-----GTGGGGTGATGGCGTGCCTTTTGA M.paratuberc.
 1016 CTT-----GTAGTGGGGTGATGGCGTGCCTTTTGA M.phlei
 947 T-----GTGGGGTGATGGCGTGCCTTTTGA M.leprae
 722 T-----GTGGGGTGATGGCGTGCCTTTTGA M.gastri
 665 C-----GTGGGGTGATGGCGTGCCTTTTGA M.kansasii
 3102 ACGTGT-----GTGGGGTGATGGCGTGCCTTTTGA M.smegmatis

690 700 710 720

1646 AGAATGAGCCTGCGAGTCAGGGACATGTGCGCAAGGTTAAC M.tuberculosis
 4 AGAATGAGCCTGCGAGTCAGGGACATGTGCGCAAGGTTAAC M.bovis
 959 AGAATGAGCCTGCGAGTCAGGGACATGTGCGCAGGTTAAC M.avium
 23 AGAATGAGCCTGCGAGTCAGGGACATGTGCGCAGGTTAAC M.intracellul
 959 AGAATGAGCCTGCGAGTCAGGGACATGTGCGCAGGTTAAC M.paratuberc.
 1046 AGAATGAGCCTGCGAGTCAGGGACATGTGCGCAGGTTAAC M.phlei
 972 AGAATGAGCCTGCGAGTCAGGGACATGTGCGCAGGTTAAC M.leprae
 747 AGAATGAGCCTGCGAGTCAGGGACATGTGCGCAGGTTAAC M.gastri
 690 AGAATGAGCCTGCGAGTCAGGGACATGTGCGCAGGTTAAC M.kansasii
 3132 AGAATGAGCCTGCGAGTCAGGGACATGTGCGCAGGTTAAC M.smegmatis

4/31

	770	780	790	800	
1726	CGACCCACACGCGCATACGCGCGTGTGAATAGTGGCGTGT				M.tuberculosis
84	CGACCCACACGCGCATACGCGCGTGTGAATAGTGGCGTGT				M.bovis
1039	CG	-----CATCCCTTTTGGGGTGT	-----	AGTGGCGTGT	M.avium
103	CG	-----CATCCCTTTTGGGGTGT	-----	AGTGGCGTGT	M.intracellular
1039	CG	-----CATCCCTTTTGGGGTGT	-----	AGTGGCGTGT	M.paratuberc.
1126	CGTAT	CAACCTGTTGGGGTTGGTGT	---	AGTGGTGTGT	M.phlei
1052	CGTAT	CACGTGTGAGCGTGTGT	-----	AGTGGCGTGT	M.leprae
827	CGTAT	CACGCGTAAGCGTGTGT	-----	AGTGGCGTGT	M.gastri
770	CGTAT	CGCGCGGAGCGTGTGT	-----	AGTGGCGTGT	M.kansasii
3212	CGTAT	CCACACAAGAGTGTGTGTGT	---	AGTGGTGTGT	M.smegmatis

	970	980	990	1000	
1926	ATTTAGGTGCAGCGTTGCGTGGTTCACCGCGGAGGTAGAG				M.tuberculosis
1228	ATTTAGGTGCAGCGTTGCGTGGTTCACCGCGGAGGTAGAG				M.avium
1228	ATTTAGGTGCAGCGTTGCGTGGTTCACCGCGGAGGTAGAG				M.paratuberc.
1322	ATTTAGGTGCAGCGT	GCATGTTTCTTAT	CGGAGGTAGAG		M.phlei
1244	ATTTAGGTGCAGCGTTGCGTGGTTCACCGCGGAGGTAGAG				M.leprae
1019	ATTTAGGTGCAGCGTTGCGTGGTTCACCGCGGAGGTAGAG				M.gastri
962	ATTTAGGTGCAGCGTTGCGTGGTTCACCGCGGAGGTAGAG				M.kansasii
3408	ATTTAGGTGCAGCGT	GCATGTTTCTTGCG	CGGAGGTAGAG		M.smegmatis

	1050	1060	1070	1080	
2005	CAGCCAAACTCCGAATGCCG-TGGTG-TA-AA-TCGTGGCA				M.tuberculosis
1307	CAGCCAAACTCCGAATGCCG-TGGTG-TAAAAGCGTGGCA				M.avium
1307	CAGCCAAACTCCGAATGCCG-TGGTG-TAAAAGCGTGGCA				M.paratuberc.
1401	CAGCCAAACTCCGAATGCCG	ATAAG	-TGAAAG	TGTGGCA	M.phlei
1323	CAGCCAAACTCCGAATGCCG-TGGT	-TAAAAGCGTGGCA			M.leprae
1098	CAGCCAAACTCCGAATGCCG-TGGTG-TATA	-GCGTGGCA			M.gastri
1041	CAGCCAAACTCCGAATGCCG-TGGTG-TATA	-GCGTGGCA			M.kansasii
3486	CAGCCAAACTCCGAATGCCG	TAAGGCAAGAG	TGCGGA		M.smegmatis

Figure 1D

00437 2241680

5/31

	1130	1140	1150	1160	
2082	ACAGCCCAGATCGCCGGCTAAGGCCCT	CAAGCGTGTGCTA	M.tuberculosis		
1385	ACAGCCCAGATCGCCGGCTAAGGCCCT	CAAGCGTGTGCTA	M.avium		
1385	ACAGCCCAGATCGCCGGCTAAGGCCCT	CAAGCGTGTGCTA	M.paratuberc.		
1479	ACAGCCCAGATCGCCGGCTAAGGCCCT	CAAGCGTGTGCTA	M.phlei		
1401	ACAGCCCAGATCGCCGGCTAAGGCCCT	CAAGCGTGTGCTA	M.leprae		
1175	ACAGCCCAGATCGCCGGCTAAGGCCCT	CAAGCGTGTGCTA	M.gastri		
1118	ACAGCCCAGATCGCCGGCTAAGGCCCT	CAAGCGTGTGCTA	M.kansasii		
3566	ACAGCCCAGATCGCCGGCTAAGGCCCT	CAAGCGTGTGCTA	M.smegmatis		

	1290	1300	1310	1320	
2241	CTCAAGCACACCGCCGAAGCCGCGGCACAT	CCACCTTGT-	M.tuberculosis		
1544	CTCAAGCACACCGCCGAAGCCGCGGCACAT	TCATCTT-TA	M.avium		
1544	CTCAAGCACACCGCCGAAGCCGCGGCACAT	TCATCTT-TA	M.paratuberc.		
1638	CTCAAGCACACCGCCGAAGCCGCGGCACAT	ATCAGCTTTG	M.phlei		
1560	CTCAAGCACACCGCCGAAGCCGCGGCACAT	CACCTTCTA	M.leprae		
1334	CTCAAGCACACCGCCGAAGCCGCGGCACAT	ACCGC--A	M.gastri		
1277	CTCAAGCACACCGCCGAAGCCGCGGCACAT	ACCGC--A	M.kansasii		
3726	TTCAAGCACACCGCCGAAGCCGCGGCACAT	GCCAACGTTTG	M.smegmatis		

	1330	1340	1350	1360	
2280	-GGTGGGTG	TGGGTAGGGGAGCGTCCCTCATT	CAGCGAAG	M.tuberculosis	
1583	CGGTGGAT	TGGGTAGGGGAGCGTCCCTCATT	CAGCGAAG	M.avium	
1583	CGGTGGAT	TGGGTAGGGGAGCGTCCCTCATT	CAGCGAAG	M.paratuberc.	
1676	TGGCTGGT	TGGGTAGGGGAGCGTCCCTCATT	CAGCGAAG	M.phlei	
1600	GGGTGGAT	TGGGTAGGGGAGCGTCCCTCATT	CAGCGAAG	M.leprae	
1367	AGGT-----	TGGGTAGGGGAGCGTCCCTCATT	CAGCGAAG	M.gastri	
1310	AGGT-----	TGGGTAGGGGAGCGTCCCTCATT	CAGCGAAG	M.kansasii	
3764	TT-----	TGGGTAGGGGAGCGTCCCTCATT	CAGCGAAG	M.smegmatis	

Figure 1E

6/31

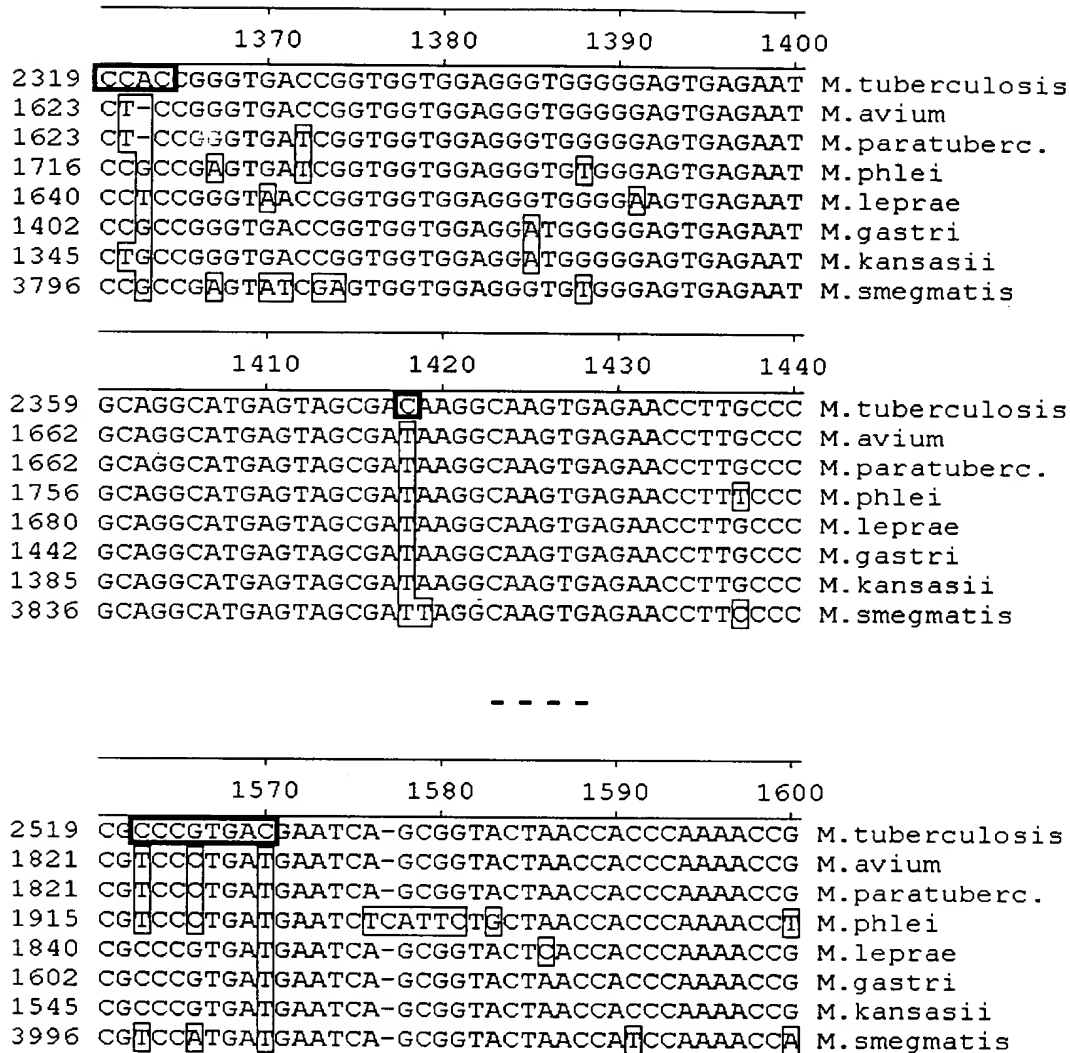


Figure 1F

1650 1660 1670 1680

2594 GGCTGCGTGGGAACCTTCGCTGGTAGTAGTCAAGCGAATGGG M.tuberculosis

1896 GGCTGCGTGGGAACCTTCGCTGGTAGTAGTCAAGCGAATGGG M.avium

1896 GGCTGCGTGGGAACCTTCGCTGGTAGTAGTCAAGCGAATGGG M.paratuberc.

1986 GGCTGCGTGGGAACCTTCGCTGGTAGTAGTCAAGCGAATGGG M.phlei

1917 GGCTGCGTGGGAACCTTCGCTGGTAGTAGTCAAGCGAATGGG M.leprae

1677 GGCTGCGTGGGAACCTTCGCTGGTAGTAGTCAAGCGAATGGG M.gastri

1620 GGCTGCGTGGGAACCTTCGCTGGTAGTAGTCAAGCGAATGGG M.kansasii

4071 GGCTGCGTGGGAACCTTCGCTGGTAGTAGTCAAGCGAATGGG M.smegmatis

Figure 1G

8/31

	1730	1740	1750	1760	
2672	-CTGGGGCAAGCC	GGTAGGG	AGAGCGATAGGCAAATCCGT		M.tuberculosis
1974	-CTGGGGCAAGCC	GTAG--	AGAGCGATAGGCAAATCCGT		M.avium
1974	-CTGGGGCAAGCC	GTAG--	AGAGCGATAGGCAAATCCGT		M.paratuberc.
2063	-C GGGG TAA CCCTGTAGGG GGAG TGATAGGCAAATCCGT				M.phlei
1995	-CTGG AG CAAGCCCGTAGGGAGAGCGATAGGCAAATCCGT				M.leprae
1755	-CTGGGGCAAGCCAGTAGGGAGAGCGATAGGCAAATCCGT				M.gastri
1698	-CTGGGGCAAGCCAGTAGGGAGAGCGATAGGCAAATCCGT				M.kansasii
4149	-C GG CG TAA GCCTGTAGGGAG TC AGATAG G TAAATCCGT				M.smegmatis

- - - -

	1970	1980	1990	2000	
2908	AGGGGG ACCGGAATAT CGTGAACACCCTTGCGGTGGGAGC				M.tuberculosis
2208	AGGGGG CCCGGAATAT CGTGAACACCCTTGCGGTGGGAGC				M.avium
2208	AGGGGG CCCGGAATAT CGTGAACACCCTTGCGGTGGGAGC				M.paratuberc.
2298	AGGGGGAC CCGTAC CGTGA GGG CT CTTGCGG GG AGC				M.phlei
2231	AGGGGG CCCGGAATAT CGTGAACACCCTTGCGGTGGGAGC				M.leprae
1910					M.gastri
1934	AGGGGGACCGGAATACCGTGAACACCCTTGCGGTGGGAGC				M.kansasii
4385	AGGGGGAC CACATGG CGT GA AG CC TT CGG CCCA AGC				M.smegmatis

- - - -

	2410	2420	2430	2440	
3345	AC CTCGACGCCAGTTGGGGC GGAGTCGTTGTTGAAATACC				M.tuberculosis
284	ACCTCGACGCCAGTTGGGGCGGAGTCGTTGTTGAAATACC				M.bovis
2645	GCACAGACGCCAGTTTGT TGGAGTCGTTGTTGAAATACC				M.avium
393	ATACAGACGCCAGTTTGTATGGAGTCGTTGTTGAAATACC				M.intracellulare
2645	GCACAGACGCCAGTTTGT TGGAGTCGTTGTTGAAATACC				M.paratuberc.
2737	GCTCGGACGCCAGTTGGGG TGGAGTCGTTGTTGAAATACC				M.phlei
2668	AC IT CGACGC T AGTTGGGG T GGAGTCGTTGTTGAAATACC				M.leprae
1910					M.gastri
2372	ACCT CA ACGCCAGTTGGGG T GGAGTCGTTGTTGAAATACC				M.kansasii
4822	GC TCAC ACGCCAGT GT GGG T GGAGTCGTTGTTGAAATACC				M.smegmatis

Figure 1H

000437 100390

9/31

	2450	2460	2470	2480	
3385	ACTCTGATCGTATTGG	GCATCTAACCTCGAACCCCTGAATC			M.tuberculosis
324	ACTCTGATCGTATTGGG	CATCTAACCTCGAACCCCTGAATC			M.bovis
2685	ACTCTGATCGTATTGG	ACACCTAACCTCGAACCCCT	TATC		M.avium
433	ACTCTGATCGTATTGG	ACACCTAACCTCGAACCCCT	TATC		M.intracellulare
2685	ACTCTGATCGTATTGG	ACACCTAACCTCGAACCCCT	TATC		M.paratuberc.
2777	ACTCTGATCGTATTGGG	CCTCTAACCTCGAACCCCTGGATC			M.phlei
2708	ACTCTGAT	CTATTGACATCTAACCTCGAACCCCTATATC			M.leprae
1910					M.gastri
2412	ACTCTGATCGTATTGG	ACACCTAACCTCGAACCCCTGAATC			M.kansasii
4862	ACTCTGATCGTATTGGG	CCTCTAACCTCGAACCCCTATATC			M.smegmatis

	2490	2500	2510	2520	
3425	GGGTTTAG	GGACAGTGCCTGGCGGGTAGTTTAACTGGGGC			M.tuberculosis
364	GGGTTTAG	GGACAGTGCCTGGCGGGTAGTTTAACTGGGGC			M.bovis
2724	GGGTTTAG	GGACAGTGCCTGGCGGGTAGTTTAACTGGGGC			M.avium
472	GGGTTTAG	GGACAGTGCCTGGCGGGTAGTTTAACTGGGGC			M.intracellulare
2724	GGGTTTAG	GGACAGTGCCTGGCGGGTAGTTTAACTGGGGC			M.paratuberc.
2817	GGGTTTAG	GGGACAGTGCCTGGCGGGTAGTTTAACTGGGGC			M.phlei
2748	GGGTTTAG	GGGACAGTGCCTGGCGGGTAGTTTAACTGGGGC			M.leprae
1910					M.gastri
2452	GGGTTTAG	GGGACAGTGCCTGGCGGGTAGTTTAACTGGGGC			M.kansasii
4902	GGGTTTAG	GGGACAGTGCCTGGCGGGTAGTTTAACTGGGGC			M.smegmatis

- - - -

	2930	2940	2950	2960	
3864	AGTACGAGAGGACCGGGACGGACGGAACCTCT	GGTGACCA			M.tuberculosis
3163	AGTACGAGAGGACCGGGACGGACGGAACCTCT	GGTATACCA			M.avium
3163	AGTACGAGAGGACCGGGACGGACGGAACCTCT	GGTATACCA			M.paratuberc.
3256	AGTACGAGAGGACCGGGACGGACGGAACCTCT	GGTATACCA			M.phlei
3187	AGTACGAGAGGACCGGGACGGACGGAACCTCT	GGTATACCA			M.leprae
1910					M.gastri
2891	AGTACGAGAGGACCGGGACGGACGGAACCTCT	AGTGACCA			M.kansasii
5342	AGTACGAGAGGACCGGGACGGACGGAACCTCT	GGTATACCA			M.smegmatis

Figure 11

00477-1009

10/31

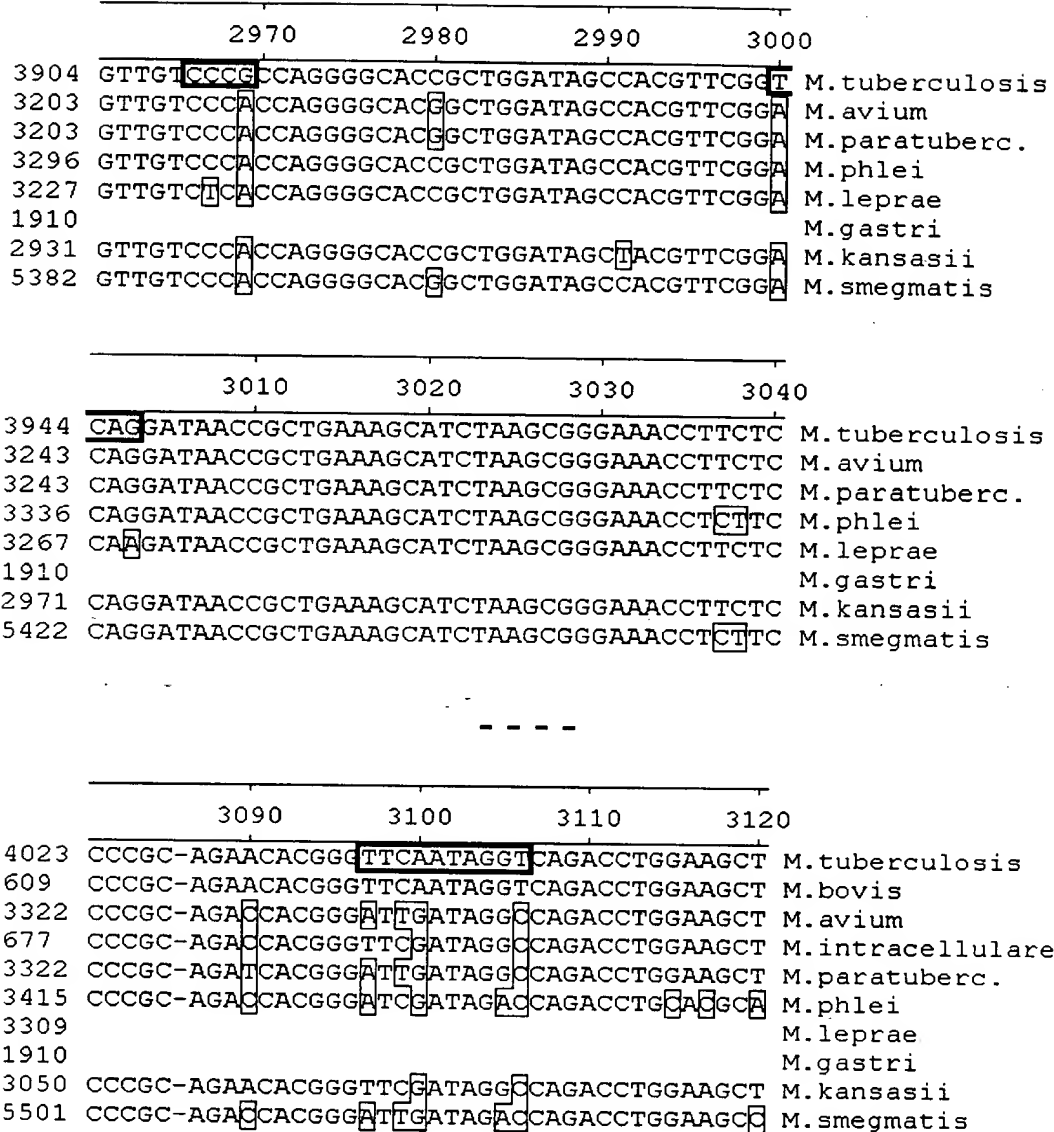


Figure 1J

	50	60	70	80	
2	GCGGCGTGCTTAACACATGCAAGTCGAACGGAAAG	GTCTC			M. tuberculosis
141	GCGGCGTGCTTAACACATGCAAGTCGAACGGAAAGGTCTC				M. bovis
39	GCGGCGTACTTAACACATGCAAGTCGAACGGAAAGG	CTC			M. avium
1	-----TTAACACATGCAAGTGAACGGAAAGAC	CC			M. intracellulare
39	GCGGCGTGCTTAACACATGCAAGTCGAACGGAAAGG	CTC			M. paratuberc.
2	GCGGCGTGCTTAACACATGCAAGTCGAACGGAAAGG	CTC			M. scrofulaceum
40	GCGGCGTGCTTAACACATGCAAGTCGAACGGAAAGGTCTC				M. leprae
2	CGGCGTGCTTAACACATGCAAGTCGAACGGAAAGGTCTC				M. kansasii
2	GCGGCGTGCTTAACACATGCAAGTCGAACGGAAAGGTCTC				M. gastri
40	GCGGCGTGCTTAACACATGCAAGTCGAACGGTAAGG	CTC			M. gordonae
1	----GTGCTTAACACATGCAAGTCGAACGGAAAGGTCTC				M. marinum

	90	100	110	120	
42	T-----TCGGAGATACTCGAGTGGCGAACGGGT				M. tuberculosis
181	T-----TCGGAGATACTCGAGTGGCGAACGGGT				M. bovis
79	T-----TCGGAGATACTCGAGTGGCGAACGGGT				M. avium
32	T-----TCGGGGTACTCGAGTGGCGAACGGGT				M. intracellulare
7	T-----TCGGAGTACTCGAGTGGCGAACGGGT				M. paratuberc.
42	T-----TCGGGGTACTCGAGTGGCGAACGGGT				M. scrofulaceum
80	TAATAATCTTTTATGAGATACTCGAGTGGCGAACGGGT				M. leprae
41	T-----TCGGAGATACTCGAGTGGCGAACGGGT				M. kansasii
42	T-----TCGGAGATACTCGAGTGGCGAACGGGT				M. gastri
80	-----GAGTACTCGAGTGGCGAACGGGT				M. gordonae
36	T-----TCGGAGATACTCGAGTGGCGAACGGGT				M. marinum

	130	140	150	160	
70	GAGTAACACGTGGGTGATCTGCCCTGCACTTC-GGGATAA				M. tuberculosis
209	GAGTAACACGTGGGTGATCTGCCCTGCACTTC-GGGATAA				M. bovis
107	GAGTAACACGTGGGCAATCTGCCCTGCACTTC-GGGATAA				M. avium
59	GAGTAACACGTGGGCAATCTGCCCTGCACTTC-GGGATAA				M. intracellulare
107	GAGTAACACGTGGGCAATCTGCCCTGCACTTC-GGGATAA				M. paratuberc.
70	GAGTAACACGTGGGCAATCTGCCCTGCACTTC-GGGATAA				M. scrofulaceum
120	GAGTAACACGTGGGTAATCTGCCCTGCACTTCGGGATAA				M. leprae
69	GAGTAACACGTGGGCAATCTGCCCTGCACAC-GGGATAA				M. kansasii
70	GAGTAACACGTGGGCAATCTGCCCTGCACAC-GGGATAA				M. gastri
104	GAGTAACACGTGGGTAATCTGCCCTGCACATC-GGGATAA				M. gordonae
64	GAGTAACACGTGGGGATCTGCCCTGCACTTC-GGGATAA				M. marinum

12/31

	170	180	190	200	
109	GCCTGGGAAACTGGGTCTAATACCGGATAGGAC	CACGGGA			M.tuberculosis
248	GCCTGGGAAACTGGGTCTAATACCGGATAGGACCACGGGA				M.bovis
146	GCCTGGGAAACTGGGTCTAATACCGGATAGGACCTCAAGA				M.avium
98	GCCTGGGAAACTGGGTCTAATACCGGATAGGACCTTTAGG				M.intracellulare
146	GCCTGGGAAACTGGGTCTAATACCGGATAGGACCTCAAGA				M.paratuberc.
109	GCCTGGGAAACTGGGTCTAATACCGGATAGGACCACTTGG				M.scrofulaceum
160	GCCTGGGAAACTGGGTCTAATACCGGATAGGACCTCAAGG				M.leprae
108	GCCTGGGAAACTGGGTCTAATACCGGATAGGACCACTTGG				M.kansasii
109	GCCTGGGAAACTGGGTCTAATACCGGATAGGACCACTTGG				M.gastri
143	GCCTGGGAAACTGGGTCTAATACCGGATAGGACCACAGGA				M.gordonae
103	GCCTGGGAAACTGGGTCTAATACCGGATAGGACCACGGGA				M.marinum

	210	220	230	240	
149	TGCATGTCTTGTGGTGGAAAGCGCTTTAGCGGTGTGGGAT				M.tuberculosis
288	TGCATGTCTTGTGGTGGAAAGCGCTTTAGCGGTGTGGGAT				M.bovis
186	CGCATGTCTTGTGGTGGAAAGCTTTTACGGTGTGGGAT				M.avium
138	CGCATGTCTTGTGGTGGAAAGCTTTTACGGTGTGGGAT				M.intracellulare
186	CGCATGTCTTGTGGTGGAAAGCTTTTACGGTGTGGGAT				M.paratuberc.
149	CGCATGTCTTGTGGTGGAAAGCTTTTACGGTGTGGGAT				M.scrofulaceum
200	CGCATGTCTTGTGGTGGAAAGCTTTTACGGTGTGGGAT				M.leprae
148	CGCATGTCTTGTGGTGGAAAGCTTTTACGGTGTGGGAT				M.kansasii
149	CGCATGTCTTGTGGTGGAAAGCTTTTACGGTGTGGGAT				M.gastri
183	CACATGTCTTGTGGTGGAAAGCTTTTACGGTGTGGGAT				M.gordonae
143	TTCATGTCTTGTGGTGGAAAGCTTTTACGGTGTGGGAT				M.marinum

	250	260	270	280	
189	GAGCCCGCGGCCTATCAGCTTGTGGTGGGGTGACGGCCT				M.tuberculosis
328	GAGCCCGCGGCCTATCAGCTTGTGGTGGGGTGACGGCCT				M.bovis
224	GAGCCCGCGGCCTATCAGCTTGTGGTGGGGTGACGGCCT				M.avium
176	GAGCCCGCGGCCTATCAGCTTGTGGTGGGGTGACGGCCT				M.intracellulare
224	GAGCCCGCGGCCTATCAGCTTGTGGTGGGGTGACGGCCT				M.paratuberc.
187	GAGCCCGCGGCCTATCAGCTTGTGGTGGGGTGACGGCCT				M.scrofulaceum
239	GAGCCCGCGGCCTATCAGCTTGTGGTGGGGTGACGGCCT				M.leprae
186	GAGCCCGCGGCCTATCAGCTTGTGGTGGGGTGACGGCCT				M.kansasii
187	GAGCCCGCGGCCTATCAGCTTGTGGTGGGGTGACGGCCT				M.gastri
221	GAGCCCGCGGCCTATCAGCTTGTGGTGGGGTGACGGCCT				M.gordonae
181	GAGCCCGCGGCCTATCAGCTTGTGGTGGGGTGACGGCCT				M.marinum

Figure 2B

13/31

	450	460	470	480	
389	AAACCTCTTT	CACCATCGACGAAGGTCCGGGTT	C	TCTCGG	M.tuberculosis
528	AAACCTCTTT	CACCATCGACGAAGGTCCGGGTT	C	TCTCGG	M.bovis
424	AAACCTCTTT	CACCATCGACGAAGGTCCGGGTT	T	TCTCGG	M.avium
376	AAACCTCTTT	CACCATCGACGAAGGTCCGGGTT	T	TCTCGG	M.intracellulare
424	AAACCTCTTT	CACCATCGACGAAGGTCCGGGTT	T	TCTAGG	M.paratuberc.
387	AAACCTCTTT	CACCATCGACGAAGGTCTCA	---	CTTGTGG	M.scrofulaceum
439	AAACCTCTTT	CACCATCGACGAAGGTCT	GGGAAT	TCTCGG	M.leprae
386	AAACCTCTTT	CACCATCGACGAAGGTCCGGGTT	C	TCTCGG	M.kansasii
387	AAACCTCTTT	CACCATCGACGAAGGTCCGGGTT	C	TCTCGG	M.gastri
420	AAACCTCTTT	CACCATCGACGAAGGTCCGGGTT	T	TCTCGG	M.gordonae
381	AAACCTCTTT	CACCATCGACGAAGGT	CGGGTT	TCTCGG	M.marinum

	1130	1140	1150	1160	
1069	TCTCATGTTGCCAGC	ACGTAATGGT	GGGGACTCGTGAGAG		M.tuberculosis
1208	TCTCATGTTGCCAGC	ACGTAATGGTGGGGACTCGTGAGAG			M.bovis
1104	TCTCATGTTGCCAGC	GGTAATGCGGGGACTCGTGAGAG			M.avium
1056	TCTCATGTTGCCAGC	GGGTAATGCGGGGACTCGTGAGAG			M.intracellulare
1098	TCTCATGTTGCCAGC	GGGTAATGCGGGGACTCGTGAGAG			M.paratuberc.
1064	TCTCATGTTGCCAGC	GGGTAATGCGGGGACTCGTGAGAG			M.scrofulaceum
1119	TCTCATGTTGCCAGC	ACGTAATGGTGGGGACTCGTGAGAG			M.leprae
1066	TCTCATGTTGCCAGC	GGGTAATGCGGGGACTCGTGAGAG			M.kansasii
1067	TCTCATGTTGCCAGC	GGGTAATGCGGGGACTCGTGAGAG			M.gastri
1100	TCTCATGTTGCCAGC	GGGTAATGCGGGGACTCGTGAGAG			M.gordonae
1061	TCTCATGTTGCCAGC	ACGTAATGGTGGGGACTCGTGAGAG			M.marinum

	1250	1260	1270	1280	
1189	CAATGGCCGGTACAAAGGGCTGCGATGCCG	CGAGGT	TAAAG		M.tuberculosis
1328	CAATGGCCGGTACAAAGGGCTGCGATGCCG	CGAGGT	TAAAG		M.bovis
1224	CAATGGCCGGTACAAAGGGCTGCGATGCCG	TAAGGT	TAAAG		M.avium
1176	CAATGGCCGGTACAAAGGGCTGCGATGCCG	TAAGGT	TAAAG		M.intracellulare
1218	CAATGGCCGGTACAAAGGGCTGCGATGCCG	TAAGGT	TAAAG		M.paratuberc.
1184	CAATGGCCGGTACAAAGGGCTGCGATGCCG	TAAGGT	TAAAG		M.scrofulaceum
1239	CAATGGCCGGTACAAAGGGCTGCGATGCCG	TAAGGT	TAAAG		M.leprae
1186	CAATGGCCGGTACAAAGGGCTGCGATGCCG	CGAGGT	TAAAG		M.kansasii
1187	CAATGGCCGGTACAAAGGGCTGCGATGCCG	CGAGGT	TAAAG		M.gastri
1220	CAATGGCCGGTACAAAGGGCTGCGATGCCG	CGAGGT	TAAAG		M.gordonae
1181	CAATGGCCGGTACAAAGGGCTGCGATGCCG	CGAGGT	TAAAG		M.marinum

Figure 2C

009437 40099

14/31

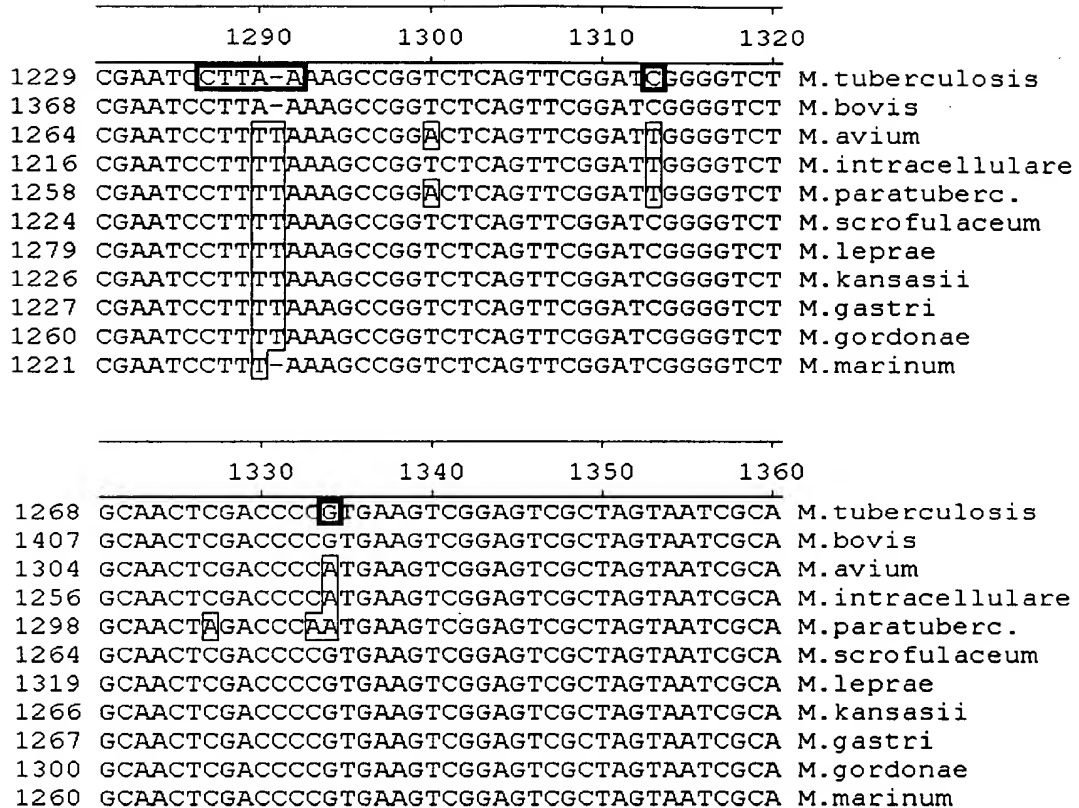


Figure 2D

15/31

50 60 70 80

128 TTCCGAACCCGGAAGCTAAGCCTGCCAGCGCCGATGATAC M.tuberculosis
39 TGCCGAACCCGGAAGCTAAGCCTGCCAGCGCCGATGATAC M.bovis
41 TCCCGAACCCGGAAGCTAAGCCTGCCAGCGCCATGATAC M.phlei
3559 TACCGAACCCGGAAGCTAAGCCTGTCAGCGCCGATGATAC M.leprae
5743 TCCCGAACCCGGAAGCTAAGCCTGCCAGCCCGATGATAC M.smegmatis

90 100 110 120

168 TGCCCTCCCGGG---TGGAAAAGTAGGACACCGCCGAAC M.tuberculosis
79 TGCCCTCCGGGG---TGGAAAAGTAGGACACCGCCGAAC M.bovis
81 TGCCCTCACCGGG---TGGAAAAGTAGGACACCGCCGAAC M.phlei
3599 TGCCCATTCGGG---TGGAAAAGTAGGACACCGCCGAAC M.leprae
5782 TACCCCTTCGGG---TGGAAAAGTAGGACACCGCCGAAC M.smegmatis

Figure 3

16/31

		90	100	110	120	
382	GGGAGCTGTCAACCGAGC	ATT	GATCCGAGGATTTCCGAAT	M.avium		
382	GGGAGCTGTCAACCGAGC	ATT	GATCCGAGGATTTCCGAAT	M.paratuberc.		
1053	GGGAGCTGTCAACCGAGC	GT	GGATCCGAGGATTTCCGAAT	M.tuberculosis		
467	GGGAGCTGTCAACCGAGC	GT	GGATCCGAGGATTTCCGAAT	M.phlei		
392	GGGAGCTGTCAACCGAGC	GT	GGATCCGAGGATTTCCGAAT	M.leprae		
167	GGGAGCTGTCAACCGAGC	GT	GGATCCGAGGATTTCCGAAT	M.gastri		
110	GGGAGCTGTCAACCGAGC	GT	GGATCCGAGGATTTCCGAAT	M.kansasii		
2548	GGGAGCTGTCAACCGAGC	GT	GGATCCGAGGATTTCCGAAT	M.smegmatis		

		170	180	190	200	
462	GAATATATAGGGTGCG-GGAGG	T	AACGCGGGGAAGTGAAA	M.avium		
462	GAATATATAGGGTGCG-GGAGG	T	AACGCGGGGAAGTGAAA	M.paratuberc.		
1133	GAATATATAGGGTGCG-GGAGG	T	AACGCGGGGAAGTGAAA	M.tuberculosis		
547	GAATATATAGG	CGTTG	-GGG	AACGCGGGGAAGTGAAA	M.phlei	
472	GAATATATAGGGT	TCG	-GGAGG	AACGCGGGGAAGTGAAA	M.leprae	
247	GAATATATAGGGTGCG-GGAGG	T	AACGCGGGGAAGTGAAA	M.gastri		
190	GAATATATAGGGTGCG-GGAGG	T	AACGCGGGGAAGTGAAA	M.kansasii		
2628	GAATATATAGG	CGTCT	-GGG	AACGCGGGAAGTGAAA	M.smegmatis	

		250	260	270	280	
541	-GTCAGTAGTGGCGAGCGAAC	C-CGGAACA	-GGCTAAACCG	M.avium		
541	-GTCAGTAGTGGCGAGCGAAC	C-CGGAACA	-GGCTAAACCG	M.paratuberc.		
1212	-GCAAGTAGTGGCGAGCGAAC	C-CGGAACA	-GGCTAAACCG	M.tuberculosis		
626	-GTSAGTAGTGGCGAGCGAA	-AGGGAGGAT	GGCTAAACCG	M.phlei		
551	-GCAAGTAGTGGCGAGCGAAC	GTGGAAAT	ATGGCTAAACCG	M.leprae		
326	-GTCAGTAGTGGCGAGCGAAC	C-CGGAACA	ATGGCTAAACCG	M.gastri		
269	-GTAAGTAGTGGCGAGCGAAC	C-CGGAACA	ATGGCTAAACCG	M.kansasii		
2706	CGTGAAGTAGTGGCGAGCGAAC	C-CGGAACA	ATGGCTAAACG	M.smegmatis		

Figure 4A

17/31

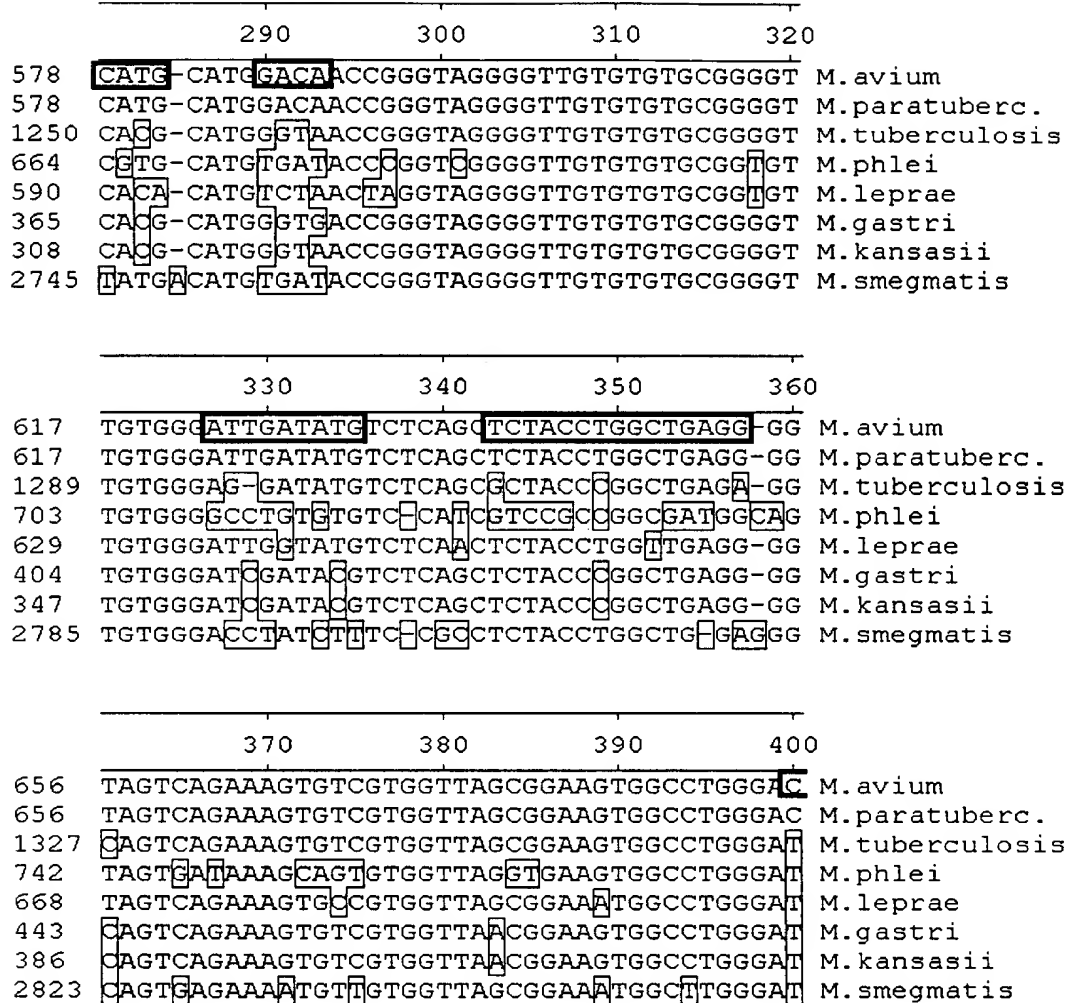


Figure 4B

18/31

	410	420	430	440	
696	GGCCC	BCCGTAGACGGTGAGAGCCC	GGTACGCGAAA-ACC		M. avium
696	GGCCCGCCGTAGACGGTGAGAGCCC	GGTACGCGAAA-ACC			M. paratuberc.
1367	GGTCTGCCGTAGACGGTGAGAGCCC	GGTACGCGAAA-ACC			M. tuberculosis
782	GGTCTGCCGTAGTGGTGAGAGCCC	GTACGCGAAA-ACC			M. phlei
708	GGCCTGCCGTAGACGGTGAGAGCCC	GTACGCGAAA-GCC			M. leprae
483	GGTCTGCCGTAGACGGTGAGAGCCC	GGTACGCGAAA-ACC			M. gastri
426	GGTCTGCCGTAGACGGTGAGAGCCC	GGTACGCGAAA-ACC			M. kansasii
2863	GGCCTGCCGTAGACGGTGAGAGCCC	GGTACGCGAAA-ACC			M. smegmatis

	450	460	470	480	
735	CGGCACCTGCCTTATATCAACA	CCCGAGTAGCAGCGGGCC			M. avium
735	CGGCACCTGCCTTATATCAACACCC	GAGTAGCAGCGGGCC			M. paratuberc.
1406	CGGCACCTGCCTTATATCAATT	CCCGAGTAGCAGCGGGCC			M. tuberculosis
820	TGCTGCCGCTGTCACAGG--	TCCCGAGTAGCAGCGGGCC			M. phlei
747	TGGCACCTGCCTTGTATCAATT	CCCGAGTAGCAGCGGGCC			M. leprae
522	CGGCACCTGCCTTGTATCAATT	CCCGAGTAGCAGCGGGCC			M. gastri
465	CGGCACCTGCCTTGTATCAATT	CCCGAGTAGCAGCGGGCC			M. kansasii
2902	CGACGTCTGTCTTGATGGTGTT	CCCGAGTAGCAGCGGGCC			M. smegmatis

- - - -

	570	580	590	600	
855	GAGGGAATGGTGAAAAGTACCCCGGG	AGGG-AGTGAAATA			M. avium
855	GAGGGAATGGTGAAAAGTACCCCGGG	AGGG-AGTGAAATA			M. paratuberc.
1526	GAGGGAATGGTGAAAAGTACCCCGGG	AGGG-AGTGAAATA			M. tuberculosis
937	GAGGGAATGGTGAAAAGTACCCCGGG	AGGG-AGTGAAATA			M. phlei
867	GAGGGAATGGTGAAAAGTACCCCGGG	AGGG-AGTGAAATA			M. leprae
642	GAGGGAATGGTGAAAAGTACCCCGGG	AGGG-AGTGAAATA			M. gastri
585	GAGGGAATGGTGAAAAGTACCCCGGG	AGGG-AGTGAAATA			M. kansasii
3022	GAGGGAATGGTGAAAAGTACCCCGGG	AGGG-AGTGAAATA			M. smegmatis

Figure 4C

19/31

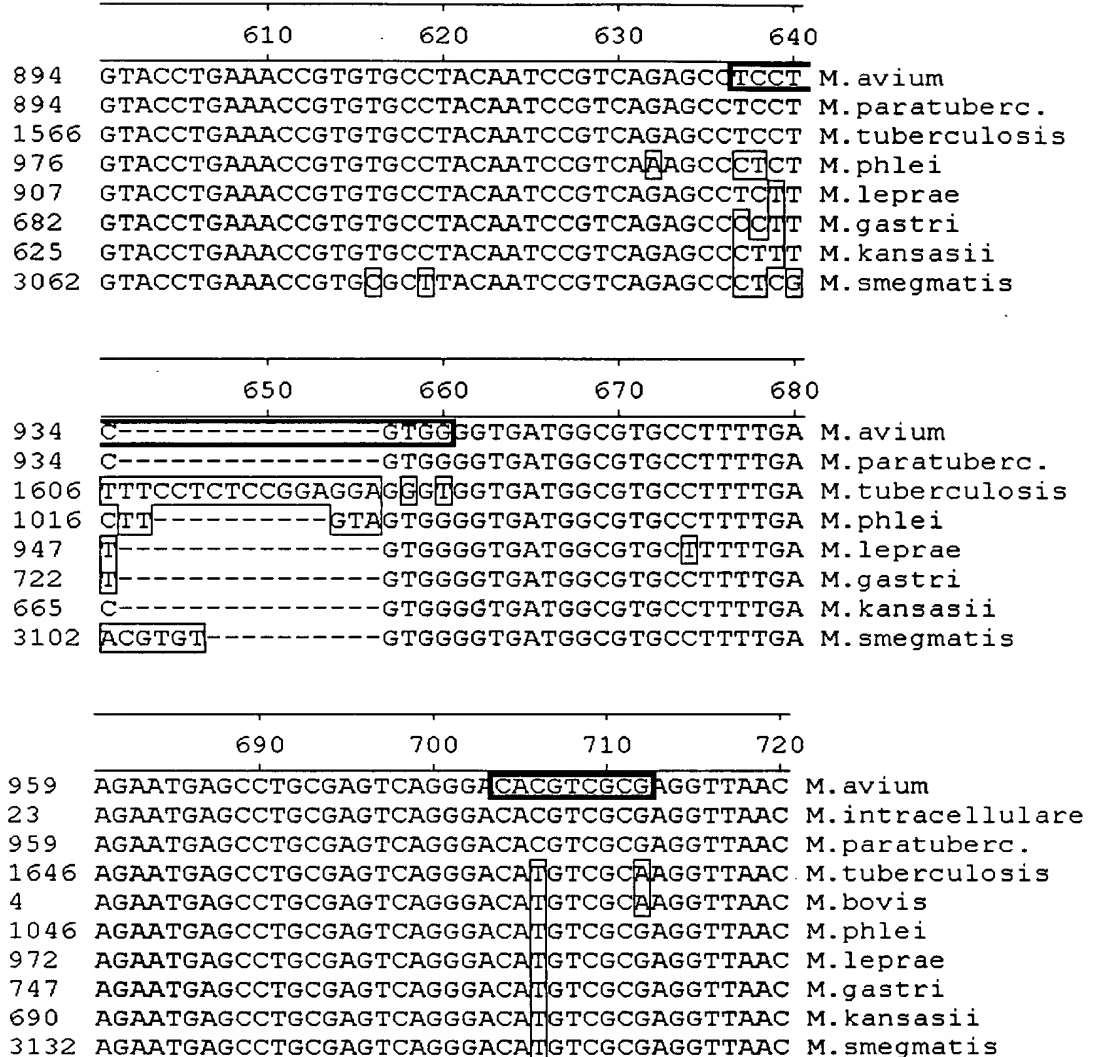


Figure 4D

20/31

770 780 790 800

1039 CGCATCCCCTTTGGG-----GTGTAGTGGCGTGT M.avium
 103 CGCATCCCCTTTGGG-----GTGTAGTGGCGTGT M.intracellulare
 1039 CGCATCCCCTTTGGG-----GTGTAGTGGCGTGT M.paratuberc.
 1726 CGACCCACACGCGCATACGCGCGTGTGAATAGTGGCGTGT M.tuberculosis
 84 CGACCCACACGCGCATACGCGCGTGTGAATAGTGGCGTGT M.bovis
 1126 CGTATCCAACCTGTT---GGGGTTGGTGTAGTGGTGTGT M.phlei
 1052 CGTATCACGCTGTGAGCGT-----GTGTAGTGGCGTGT M.leprae
 827 CGTATCACGCGTAAGCGT-----GTGTAGTGGCGTGT M.gastri
 770 CGTATCGCGCGGAGCGT-----GTGTAGTGGCGTGT M.kansasii
 3212 CGTATCCACACAAGAGTGTGTG---GTGTAGTGGTGTGT M.smegmatis

1050 1060 1070 1080

1307 CAGCCAAACTCCGAATGCCG-TGGTG-TAAAAGCGTGGCA M.avium
 1307 CAGCCAAACTCCGAATGCCG-TGGTG-TAAAAGCGTGGCA M.paratuberc.
 2005 CAGCCAAACTCCGAATGCCG-TGGTG-TA-AAGCGTGGCA M.tuberculosis
 1401 CAGCCAAACTCCGAATGCCGATAAG-TGAAAGTGTGGCA M.phlei
 1323 CAGCCAAACTCCGAATGCCG-TGGT-TAAAAGCGTGGCA M.leprae
 1098 CAGCCAAACTCCGAATGCCG-TGGTG-TATA-GCGTGGCA M.gastri
 1041 CAGCCAAACTCCGAATGCCG-TGGTG-TATA-GCGTGGCA M.kansasii
 3486 CAGCCAAACTCCGAATGCCGTAAGGCCAAGAGTGGGA M.smegmatis

1170 1180 1190 1200

1425 AGTGGAAAAGGATGTGTAGTCGCAGAGACAACCAGGAGG M.avium
 1425 AGTGGAAAAGGATGTGTAGTCGCAGAGACAACCAGGAGG M.paratuberc.
 2122 AGTGGAAAAGGATGTGTAGTCGCAGAGACAACCAGGAGG M.tuberculosis
 1519 AGTGGAAAAGGATGTGTAGTCGCAGAGACAACCAGGAGG M.phlei
 1441 AGTGGAAAAGGATGTGTAGTCGCAGAGACAACCAGGAGG M.leprae
 1215 AGTGGAAAAGGATGTGTAGTCGCAGAGACAACCAGGAGG M.gastri
 1158 AGTGGAAAAGGATGTGTAGTCGCAGAGACAACCAGGAGG M.kansasii
 3606 AGTGGAAAAGGATGTGTAGTCGCAGAGAGACAACCAGGAGG M.smegmatis

Figure 4E

009437 100397

21/31

	1250	1260	1270	1280	
1504	CTCACTGGTCAAGTGATT	ATGCGCC	BATAATGTAGCGGGG		M.avium
1504	CTCACTGGTCAAGTGATT	ATGCGCCGATAATGTAGCGGGG			M.paratuberc.
2201	CTCACTGGTCAAGTGATT	GTGCGCCGATAATGTAGCGGGG			M.tuberculosis
1598	CTCACTGGTCAAGTGATT	GTGCGC	IGATAATGTAGCGGGG		M.phlei
1520	CTCACTGGTCAAGTGATT	GTGCGCCGATAATGTAGCGGGG			M.leprae
1294	CTCACTGGTCAAGTGATT	GTGCGCCGATAATGTAGCGGGG			M.gastri
1237	CTCACTGGTCAAGTGATT	GTGCGCCGATAATGTAGCGGGG			M.kansasii
3686	ITCACTGGTCAAGTGATT	GTGCGCCGATA	ITGTG	GGCGGG	M.smegmatis

	1290	1300	1310	1320	
1544	CTCAAGCACACCGCCGAAGCCGCGGCACAT	TCATCTT-TA			M.avium
1544	CTCAAGCACACCGCCGAAGCCGCGGCACAT	TCATCTT-TA			M.paratuberc.
2241	CTCAAGCACACCGCCGAAGCCGCGGCACAT	CACTTGT			M.tuberculosis
1638	CTCAAGCACACCGCCGAAGCCGCGGCA	ATCAGCCTTTG			M.phlei
1560	CTCAAGCACACCGCCGAAGCCGCGGCACAT	TCACCTTCTA			M.leprae
1334	CTCAAGCACACCGCCGAAGCCGCGACA	-----ACCGC	-----A		M.gastri
1277	CTCAAGCACACCGCCGAAGCCGCGACA	-----ACCGC	-----A		M.kansasii
3726	ITCAAGCACACCGCCGAAGCCGCGGA	-----GCCAACGTTTG			M.smegmatis

	1330	1340	1350	1360	
1583	CGGTGGATGTGGGTAGGGGAGCGT	CCCC	CATTCAGCGAAG		M.avium
1583	CGGTGGATGTGGGTAGGGGAGCGT	CCCCCATTCAGCGAAG			M.paratuberc.
2280	GGTGGGTGTGGGTAGGGGAGCGT	CCCCCATTCAGCGAAG			M.tuberculosis
1676	TGGCTGGTGTGGGTAGGGGAGCGT	CCCATTCAGCGAAG			M.phlei
1600	GGGTGGATGTGGGTAGGGGAGCGT	CCCATTCAGCGAAG			M.leprae
1367	AGGT-----TGGGTAGGGGAGCGT	CCCCCATTCAGCGAAG			M.gastri
1310	AGGT-----TGGGTAGGGGAGCGT	CCCCCATTCAGCGAAG			M.kansasii
3764	TT-----TGGGTAGGGGAGCGT	CCCATTCAGCGAAG			M.smegmatis

Figure 4F

22/31

1370 1380 1390 1400

1623 CT-CGGGTGACCGGTGGTGGAGGGTGGGGGAGTGAGAAT M.avium
 1623 CT-CCGGGTGA^TCGGTGGTGGAGGGTGGGGGAGTGAGAAT M.paratuberc.
 2319 CCACCGGGTGACCGGTGGTGGAGGGTGGGGGAGTGAGAAT M.tuberculosis
 1716 CCGCCG^AGTGA^TCGGTGGTGGAGGGT^TGGGAGTGAGAAT M.phlei
 1640 CCTCCGGGT^AACCGGTGGTGGAGGGTGGGG^AAGTGAGAAT M.leprae
 1402 CCGCCGGGTGACCGGTGGTGGAGG^ATGGGGGAGTGAGAAT M.gastri
 1345 CT^TCCGGGTGACCGGTGGTGGAGG^ATGGGGGAGTGAGAAT M.kansasii
 3796 CCGCCG^AGTAT^CGAGTGGTGGAGGGT^TGGGAGTGAGAAT M.smegmatis

1530 1540 1550 1560

1781 CGATGGACAACGGGTTGATATTCCCGTACCCGTGTATGGG M.avium
 1781 CGATGGACAACGGGTTGATATTCCCGTACCCGTGTATGGG M.paratuberc.
 2479 CGATGGACAACGGGTTGATATTCCCGTACCCGTGT^TTGGG M.tuberculosis
 1875 CGATGGACAACGGGTTGATATTCCCGTACCCGTGTATG^AG M.phlei
 1800 CGATGGACAACGGGTTGATATTCCCGTACCCGTGT^TTG^TG M.leprae
 1562 CGATGGACAACGGGTTGATATTCCCGTACCCGTGT^TTGGG M.gastri
 1505 CGATGGACAACGGGTTGATATTCCCGTACCCGTGT^TTGGG M.kansasii
 3956 CGATGGACAACGGGTTGATATTCCCGTACCCGTGTATG^TG M.smegmatis

1570 1580 1590 1600

1821 CGTCCCTGAT^AGAATCA-GCGGTACTAACCACCCAAAACCG M.avium
 1821 CGTCCCTGATGAATCA-GCGGTACTAACCACCCAAAACCG M.paratuberc.
 2519 CG^CCC^TGTGA^CGAATCA-GCGGTACTAACCACCCAAAACCG M.tuberculosis
 1915 CGTCCCTGATGAATC^TCATT^CT^GCTAACCACCCAAAACCG^T M.phlei
 1840 CG^CCC^TGTGAATCA-GCGGTACT^AACCACCCAAAACCG M.leprae
 1602 CG^CCC^TGTGAATCA-GCGGTACTAACCACCCAAAACCG M.gastri
 1545 CG^CCC^TGTGAATCA-GCGGTACTAACCACCCAAAACCG M.kansasii
 3996 CGTCCATGATGAATCA-GCGGTACTAACCA^TCCAAAACCG^A M.smegmatis

Figure 4G

CGG4377.10099

23/31

1610 1620 1630 1640

1860 GAT-CGATCCAT-TCCCCTTCGGGGG-C-GTGGCGATT-CGG M.avium
 1860 GAT-CGACCAT-TCCCCTTCGGGGGC-GTGGCGATT-CGG M.paratuberc.
 2558 GAT-CGATCAC-TCCCCTTCGGGGG-TGTGGAGGTTG-TGG M.tuberculosis
 1955 GGC-CGATC--ATCC--TTCGGGG--GTGACGGTTG-GG M.phlei
 1879 GAT-CGACCATATCCCCTTCGGGGGCTATGGAGGTT-CGG M.leprae
 1641 GAT-CGATCAC-TCCCCTTCGGGGGA-GTGGAGGTC-TGG M.gastri
 1584 GAT-CGATCAC-TCCCCTTCGGGGGC-GTGGAGGTC-TGG M.kansasii
 4035 ACCGTGACCGCACCT--TTCGGGG--TGTGGCGTTGGTGG M.smegmatis

1650 1660 1670 1680

1896 GGCTGCGTGGGACCTTCGCTGGTAGTAGTCAAGCAATGGG M.avium
 1896 GGCTGCGTGGGACCTTCGCTGGTAGTAGTCAAGCAATGGG M.paratuberc.
 2594 GGCTGCGTGGGAACCTTCGCTGGTAGTAGTCAAGCAATGGG M.tuberculosis
 1986 GGCTGCGTGGGACCG-GTGGGTAGTAGTCAAGCGATGGG M.phlei
 1917 GGCTGCGTGGGAACCTTCGTTGGTAGTAGTCAAGCGATGGG M.leprae
 1677 GGCTGCGTGGGACCTTCGCTGGTAGTAGTCAAGCGATGGG M.gastri
 1620 GGCTGCGTGGGACCTTCGCTGGTAGTAGTCAAGCGATGGG M.kansasii
 4071 GGCTGCGATGGGACCTTCGTTGGTAGTAGTCAAGCGATGGG M.smegmatis

1690 1700 1710 1720

1936 -GTGACGCAGGAAGGCAGCCGTACCAGTCAGTGGTAATA- M.avium
 1936 -GTGACGCAGGAAGGCAGCCGTACCAGTCAGTGGTAATA- M.paratuberc.
 2634 -GTGACGCAGGAAGGTAGCCGTACCAGTCAGTGGTAATA- M.tuberculosis
 2025 -GTGACGCAGGAAGGTAGCCGTACCAGTCAGTGGTAATA- M.phlei
 1957 -GTGACGCAGGAAGGTAGCCGTACCAGTCAGTGGTAATA- M.leprae
 1717 -GTGACGCAGGAAGGCAGCCGTACCAGTCAGTGGTAATA- M.gastri
 1660 -GTGACGCAGGAAGGCAGCCGTACCAGTCAGTGGTAATA- M.kansasii
 4111 -GTGACGCAGGAAGGTAGCCGTACCAGTCAGTGGTAATA- M.smegmatis

1730 1740 1750 1760

1974 -CTGGGGCAAGCCCGTAG--AGAGCGATAGGCAAATCCGT M.avium
 1974 -CTGGGGCAAGCCCGTAG--AGAGCGATAGGCAAATCCGT M.paratuberc.
 2672 -CTGGGGCAAGCCCGTAGGGAGAGCGATAGGCAAATCCGT M.tuberculosis
 2063 -CTGGGGTAAACCTGTAGGGGAGTGATAGGCAAATCCGT M.phlei
 1995 -CTGGAGCAAGCCCGTAGGGAGAGCGATAGGCAAATCCGT M.leprae
 1755 -CTGGGGCAAGCCAGTAGGGAGAGCGATAGGCAAATCCGT M.gastri
 1698 -CTGGGGCAAGCCAGTAGGGAGAGCGATAGGCAAATCCGT M.kansasii
 4149 -CTGGCGTAAGCCGTAGGGAGTCAGATAGGTAATCCGT M.smegmatis

Figure 4H

0894377.100307

24/31

	1810	1820	1830	1840	
2051	CG-AATTCGGTGATCCTCTGCTGCCAAGAAAAGCCTCTA-				M.avium
2051	CG-AATTCGGTGATCCTCTGCTGCCAAGAAAAGCCTCTA-				M.paratuberc.
2751	CG-AATTCGGTGATCCTCTGCTGCCAAGAAAAGCCTCTA-				M.tuberculosis
2141	CG-AATTCGGTGATCCTCTGCTGCCAAGAAAAGCCTCTA-				M.phlei
2074	CG-AATTCGGTGATCCTCTGCTGCCAAGAAAAGCCTCTA-				M.leprae
1834	CG-AATTCGGTGATCCTCTGCTGCCAAGAAAAGCCTCTA-				M.gastri
1777	CG-AATTCGGTGATCCTCTGCTGCCAAGAAAAGCCTCTA-				M.kansasii
4228	CG-AATTCGGTGATCCTCTGCTGCCAAGAAAAGCCTCTA-				M.smegmatis
	1850	1860	1870	1880	
2089	GCGAGCACATACACGCGCCCGTACCCCAAACCAACACAGGT				M.avium
2089	GCGAGCACATACACGCGCCCGTACCCCAAACCAACACAGGT				M.paratuberc.
2789	GCGAGCACACACACGCGCCCGTACCCCAAACCAACACAGGT				M.tuberculosis
2179	GCGAGCACACACACGCGCCCGTACCCCAAACCAACACAGGT				M.phlei
2112	GCGAGCACACACACGCGCCCGTACCCCAAACCAACACAGGT				M.leprae
1872	GCGAGCACACACACGCGCCCGTACCCCAAACCAACACAGGT				M.gastri
1815	GCGAGCACACACACGCGCCCGTACCCCAAACCAACACAGGT				M.kansasii
4266	GCGAGCACACACACGCGCCCGTACCCCAAACCAACACAGGT				M.smegmatis

	1970	1980	1990	2000	
2208	AGGGGGGACCGGAATACCGTGAACACCCTTGCGGTGGGAGC				M.avium
2208	AGGGGGGACCGGAATACCGTGAACACCCTTGCGGTGGGAGC				M.paratuberc.
2908	AGGGGGGACCGGAATACCGTGAACACCCTTGCGGTGGGAGC				M.tuberculosis
2298	AGGGGGGACCGGAATACCGTGAACACCCTTGCGGTGGGAGC				M.phlei
2231	AGGGGGGACCGGAATACCGTGAACACCCTTGCGGTGGGAGC				M.leprae
1910					M.gastri
1934	AGGGGGGACCGGAATACCGTGAACACCCTTGCGGTGGGAGC				M.kansasii
4385	AGGGGGGACCGGAATACCGTGAACACCCTTGCGGTGGGAGC				M.smegmatis
	2010	2020	2030	2040	
2248	GGGATTCGGTCGCAGAAACCAAGTGGGTAGCGACT-GTTTA				M.avium
2248	GGGATTCGGTCGCAGAAACCAAGTGGGTAGCGACT-GTTTA				M.paratuberc.
2948	GGGATTCGGTCGCAGAAACCAAGTGGGTAGCGACT-GTTTA				M.tuberculosis
2338	GGGATTCGGTCGCAGAAACCAAGTGGGTAGCGACT-GTTTA				M.phlei
2271	GGGATTCGGTCGCAGAAACCAAGTGGGTAGCGACT-GTTTA				M.leprae
1910					M.gastri
1974	GGGATTCGGTCGCAGAAACCAAGTGGGTAGCGACT-GTTTA				M.kansasii
4425	GGGATTCGGTCGCAGAAACCAAGTGGGTAGCGACT-GTTTA				M.smegmatis

Figure 4I

25/31

	2130	2140	2150	2160	
2367	CCGTTAACCC	GT	--AAGGGTGAAGCGGAGAATTTAAGCCC		M.avium
2367	CCGTTAACCCGT	--AAGGGTGAAGCGGAGAATTTAAGCCC			M.paratuberc.
3067	CCGTTAACCCG	--AAGGGTGAAGCGGAGAATTTAAGCCC			M.tuberculosis
2457	CCGTTAACCC	TTTCGG	GGGTGAAGCGGAGAATTTAAGCCC		M.phlei
2390	CGTTAACCCGA	--AAGGGTGAAGCGGAGAATTTAAGCCC			M.leprae
1910					M.gastri
2094	CCGTTAACCCG	--AAGGGTGAAGCGGAGAATTTAAGCCC			M.kansasii
4544	CCGTTAACCC	CCTTGG	GGGTGAAGCGGAGAATTTAAGCCC		M.smegmatis

- - - -

	2250	2260	2270	2280	
2485	GTAACGACTTC	CCAA	TTGTCTCAACCATAGACTCGGCGAA		M.avium
2485	GTAACGACTTCCCA	ACTGTCTCAACCATAGACTCGGCGAA			M.paratuberc.
3185	GTAACGACTTCT	CAACTGTCTCAACCATAGACTCGGCGAA			M.tuberculosis
2577	GTAACGACTTCT	CAACTGTCTCAACCATAGACTCGGCGAA			M.phlei
2508	GTAACGACTTCT	CAACTGTCTCAACCATAGACTCGGCGAA			M.leprae
1910					M.gastri
2212	GTAACGACTTCT	CAACTGTCTCAACCATAGACTCGGCGAA			M.kansasii
4663	GTAACGACTTCT	CAACTGTCTCAAC	ATAGACTCGGCGAA		M.smegmatis

- - - -

	2370	2380	2390	2400	
2605	GTTTCGGTACGGTTTGTGTAGGATAGGTGGGAGACT	TTGAA			M.avium
2605	GTTTCGGTACGGTTTGTGTAGGATAGGTGGGAGACTTTGAA				M.paratuberc.
3305	GTTTCGGTACGGTTTGTGTAGGATAGGTGGGAGACT	GTGAA			M.tuberculosis
2697	GTCGATACGGTTTGTGTAGGATAGGTGGGAGACT	GTGAA			M.phlei
2628	GTTTCGGTTCGGTTTGTGTAGGATAGGTGGGAGACT	GTGAA			M.leprae
1910					M.gastri
2332	GTTTCGGTACGGTTTGTGTAGGATAGGTGGGAGACT	GTGAA			M.kansasii
4782	GTCGATACGGTTTGTGTAGGATAGGTGGGAGACT	GTGAA			M.smegmatis

Figure 4J

GenBank Entry

26/31

	2410	2420	2430	2440	
2645	GCACAGACGCCAGTTTGTGTGGAGTCGTTGTTGAAATACC				M.avium
393	ATACAGACGCCAGTTTGTGTGGAGTCGTTGTTGAAATACC				M.intracellulare
2645	GCACAGACGCCAGTTTGTGTGGAGTCGTTGTTGAAATACC				M.paratuberc.
3345	ACCTCGACGCCAGTTGGGGGGAGTCGTTGTTGAAATACC				M.tuberculosis
284	ACCTCGACGCCAGTTGGGGGGAGTCGTTGTTGAAATACC				M.bovis
2737	GCTCGACGCCAGTTGGGGGGAGTCGTTGTTGAAATACC				M.phlei
2668	ACTTCGACGCTAGTTGGGGGGAGTCGTTGTTGAAATACC				M.leprae
1910					M.gastri
2372	ACCTCAACGCCAGTTGGGGGGAGTCGTTGTTGAAATACC				M.kansasii
4822	GCTCAACGCCAGTTGGGGGGAGTCGTTGTTGAAATACC				M.smegmatis

	2450	2460	2470	2480	
2685	ACTCTGATCGTATTGGACACCTAACGTCGAACCCT-TATC				M.avium
433	ACTCTGATCGTATTGGACACCTAACGTCGAACCCT-TATC				M.intracellulare
2685	ACTCTGATCGTATTGGACACCTAACGTCGAACCCT-TATC				M.paratuberc.
3385	ACTCTGATCGTATTGGGCATCTAACCTCGAACCCTGAATC				M.tuberculosis
324	ACTCTGATCGTATTGGGCATCTAACCTCGAACCCTGAATC				M.bovis
2777	ACTCTGATCGTATTGGGCCTCTAACCTCGGACCGTGGATC				M.phlei
2708	ACTCTGATCTGATTGACATCTAACCTCGAACCCTATATC				M.leprae
1910					M.gastri
2412	ACTCTGATCGTATTGGACACCTAACGTCGAACCCTGAATC				M.kansasii
4862	ACTCTGATCGTATTGGGCCTCTAACCTCGGACCGTATATC				M.smegmatis

- - - -

	2690	2700	2710	2720	
2924	GGTGTCTCTCAACGGATAAAAGGTACCCCGGGGATAACGG				M.avium
2924	GGTGTCACTCAACGGATAAAAGGTACCCCGGGGATAACAG				M.paratuberc.
3625	GGTGTCTCTCAACGGATAAAAGGTACCCCGGGGATAACAG				M.tuberculosis
3017	GGTGTCTCTCAACGGATAAAAGGTACCCCGGGGATAACAG				M.phlei
2948	GGTGTCTCTCAACGGATAAAAGGTACCCCGGGGATAACAG				M.leprae
1910					M.gastri
2652	GGTGTCTCTCAACGGATAAAAGGTACCCCGGGGATAACAG				M.kansasii
5102	GGTGTCTCTCAACGGATAAAAGGTACCCCGGGGATAACAG				M.smegmatis

	2730	2740	2750	2760	
2964	GCTGATCTTCCCCAAGAGTCCATATCGACGGGATGGTTTG				M.avium
2964	GCTGATCTTCCCCAAGAGTCCATATCGACGGGATGGTTTG				M.paratuberc.
3665	GCTGATCTTCCCCAAGAGTCCATATCGACGGGATGGTTTG				M.tuberculosis
3057	GCTGATCTTCCCCAAGAGTCCATATCGACGGGATGGTTTG				M.phlei
2988	GCTGATCTTCCCCAAGAGTCCATATCGACGGGATGGTTTG				M.leprae
1910					M.gastri
2692	GCTGATCTTCCCCAAGAGTCCATATCGACGGGATGGTTTG				M.kansasii
5142	GCTGATCTTCCCCAAGAGTCCATATCGACGGGATGGTTTG				M.smegmatis

Figure 4K

26E00T 44E4680

27/31

	2770	2780	2790	2800	
3004	GCACCTCGATGTCGGCTCGTCGCATCCTGGGGCTGGAGCA				M. avium
3004	GCACCTCGATGTCGGCTCGTCGCATCCTGGGGCTGGAGCA				M. paratuberc.
3705	GCACCTCGATGTCGGCTCGTCGCATCCTGGGGCTGGAGCA				M. tuberculosis
3097	GCACCTCGATGTCGGCTCGTCGCATCCTGGGGCTGGAGCA				M. phlei
3028	GCACCTCGATGTCGGCTCGTCGCATCCTGGGGCTGGAGCA				M. leprae
1910					M. gastri
2732	GCACCTCGATGTCGGCTCGTCGCATCCTGGGGCTGGAGCA				M. kansasii
5182	GCACCTCGATGTCGGCTCGTCGCATCCTGGGGCTGGAGCA				M. smegmatis
	2810	2820	2830	2840	
3044	GGTCCCAAGGGTTGGGCTGTTGCGCC-ATTAAAGCGGCAC				M. avium
3044	GGTCCCAAGGGTTGGGCTGTTGCGCC-ATTAAAGCGGCAC				M. paratuberc.
3745	GGTCCCAAGGGTTGGGCTGTTGCGCC-ATTAAAGCGGCAC				M. tuberculosis
3137	GGTCCCAAGGGTTGGGCTGTTGCGCC-ATTAAAGCGGCAC				M. phlei
3068	GGTCCCAAGGGTTGGGCTGTTGCGCC-ATTAAAGCGGCAC				M. leprae
1910					M. gastri
2772	GGTCCCAAGGGTTGGGCTGTTGCGCC-ATTAAAGCGGCAC				M. kansasii
5222	GGTCCCAAGGGTTGGGCTGTTGCGCC-ATTAAAGCGGCAC				M. smegmatis
- - - -					
	3050	3060	3070	3080	
3283	CAAGATCAGGTTT-CTCACCCCTTTTAGAGGGGATAAGGCC				M. avium
638	CAAGATCAGGTTT-CTCACCCCTTTTAGAGGGGATAAGGCC				M. intracellulare
3283	CAAGATCAGGTTT-CTCACCCCTTTTAGAGGGGATAAGGCC				M. paratuberc.
3984	CAAGATCAGGTTT-CTCACCCCTTTTAGAGGGGATAAGGCC				M. tuberculosis
570	CAAGATCAGGTTT-CTCACCCCTTTTAGAGGGGATAAGGCC				M. bovis
3376	CAAGATCAGGTTT-CTCACCCCTTTTAGAGGGGATAAGGCC				M. phlei
3307	CAA				M. leprae
1910					M. gastri
3011	CAAGATCAGGTTT-CTCACCCCTTTTAGAGGGGATAAGGCC				M. kansasii
5462	CAAGATCAGGTTT-CTCACCCCTTTTAGAGGGGATAAGGCC				M. smegmatis
	3090	3100	3110	3120	
3322	CCCGC-AGACCACGGGATTGATAGGCCAGACCTGGAAGCT				M. avium
677	CCCGC-AGACCACGGGATTGATAGGCCAGACCTGGAAGCT				M. intracellulare
3322	CCCGC-AGACCACGGGATTGATAGGCCAGACCTGGAAGCT				M. paratuberc.
4023	CCCGC-AGACCACGGGATTGATAGGCCAGACCTGGAAGCT				M. tuberculosis
609	CCCGC-AGACCACGGGATTGATAGGCCAGACCTGGAAGCT				M. bovis
3415	CCCGC-AGACCACGGGATTGATAGGCCAGACCTGGAAGCT				M. phlei
3309					M. leprae
1910					M. gastri
3050	CCCGC-AGACCACGGGATTGATAGGCCAGACCTGGAAGCT				M. kansasii
5501	CCCGC-AGACCACGGGATTGATAGGCCAGACCTGGAAGCT				M. smegmatis

Figure 4L

0894377-100397

28/31

	130	140	150	160	
107	GAGTAACACGTGGG	CAATCTGCCCTGCACTTC	-GGGATAA	M.avium	
59	GAGTAACACGTGGGCAATCT	GCCCTGCACTTC	-GGGATAA	M.intracellulare	
107	GAGTAACACGTGGGCAATCT	ACCCTGCACTTC	-GGGATAA	M.paratuberc.	
70	GAGTAACACGTGGGCAATCT	GCCCTGCACTTC	-GGGATAA	M.scrofulaceum	
70	GAGTAACACGTGGG	TGATCTGCCCTGCACTTC	-GGGATAA	M.tuberculosis	
209	GAGTAACACGTGGG	TGATCTGCCCTGCACTTC	-GGGATAA	M.bovis	
120	GAGTAACACGTGGG	TAATCTGCCCTGCACTTC	AGGGATAA	M.leprae	
69	GAGTAACACGTGGGCAATCT	GCCCTGCACACC	-GGGATAA	M.kansasii	
70	GAGTAACACGTGGGCAATCT	GCCCTGCACACC	-GGGATAA	M.gastri	
104	GAGTAACACGTGGG	TAATCTGCCCTGCACATC	-GGGATAA	M.gordonae	
64	GAGTAACACGTGGG	CAATCTGCCCTGCACTTC	-GGGATAA	M.marinum	
- - - -					
	450	460	470	480	
424	AAACCTCTTTTACC	ATCGACGAAGGTCCGGG	TTTT	CTCGG	M.avium
376	AAACCTCTTTTACC	ATCGACGAAGGTCCGGG	TTTTCT	CTCGG	M.intracellulare
424	AAACCTCTTTTACC	ATCGACGAAGGTCCGGG	TTTTCT	AGG	M.paratuberc.
387	AAACCTCTTTTACC	ATCGACGAAGGTCTCA	--CTTT	GTGG	M.scrofulaceum
389	AAACCTCTTTTACC	ATCGACGAAGGTCCGGG	TTCT	CTCGG	M.tuberculosis
528	AAACCTCTTTTACC	ATCGACGAAGGTCCGGG	TTCT	CTCGG	M.bovis
439	AAACCTCTTTTACC	ATCGACGAAGGTCT	GGGAA	TTCT	CTCGG
386	AAACCTCTTTTACC	ATCGACGAAGGTCCGGG	TTCT	CTCGG	M.kansasii
387	AAACCTCTTTTACC	ATCGACGAAGGTCCGGG	TTCT	CTCGG	M.gastri
420	AAACCTCTTTTACC	ATCGACGAAGGTCCGGG	TTTTCT	CTCGG	M.gordonae
381	AAACCTCTTTTACC	ATCGACGAAGGT	TCGGG	TTTTCT	CTCGG
- - - -					
	490	500	510	520	
429	ATTGACGGTAGGTGGAGAAGAAGC	ACCGGCCAACTACGTG			M.tuberculosis
568	ATTGACGGTAGGTGGAGAAGAAGC	ACCGGCCAACTACGTG			M.bovis
464	ATTGACGGTAGGTGGAGAAGAAGC	ACCGGCCAACTACGTG			M.avium
416	ATTGACGGTAGGTGGAGAAGAAGC	ACCGGCCAACTACGTG			M.intracellulare
464	ATTGACGGTAGGTGGAGAAGAAGC	ACCGGCCAACTACGTG			M.paratuberc.
424	ATTGACGGTAGGTGGAGAAGAAGC	ACCGGCCAACTACGTG			M.scrofulaceum
479	ATTGACGGTAGGTGGAGAAGAAGC	ACCGGCCAACTACGTG			M.leprae
426	ATTGACGGTAGGTGGAGAAGAAGC	ACCGGCCAACTACGTG			M.kansasii
427	ATTGACGGTAGGTGGAGAAGAAGC	ACCGGCCAACTACGTG			M.gastri
460	ATTGACGGTAGGTGGAGAAGAAGC	ACCGGCCAACTACGTG			M.gordonae
421	ATTGACGGTAGGTGGAGAAGAAGC	ACCGGCCAACTACGTG			M.marinum

Figure 5A

29/31

	1130	1140	1150	1160	
1104	TCTCATGTTGCCAG	GGGTAATGC	GGGGGACTCGTGAGAG		M.avium
1056	TCTCATGTTGCCAGCGGGTAATGCCGGGGACTCGTGAGAG				M.intracellulare
1098	TCTCATGTTGCCAGCGGGTAATGC	GGGGGACTCGTGAGAG			M.paratuberc.
1064	TCTCATGTTGCCAGCGGGTAATGCCGGGGACTCGTGAGAG				M.scrofulaceum
1069	TCTCATGTTGCCAGCACGTAATG	STGGGGGACTCGTGAGAG			M.tuberculosis
1208	TCTCATGTTGCCAGCACGTAATG	STGGGGGACTCGTGAGAG			M.bovis
1119	TCTCATGTTGCCAGCACGTAATG	STGGGGGACTCGTGAGAG			M.leprae
1066	TCTCATGTTGCCAGCGGGTAATGCCGGGGACTCGTGAGAG				M.kansasii
1067	TCTCATGTTGCCAGCGGGTAATGCCGGGGACTCGTGAGAG				M.gastri
1100	TCTCATGTTGCCAGCGGGTAATGCCGGGGACTCGTGAGAG				M.gordonae
1061	TCTCATGTTGCCAGCACGTAATG	STGGGGGACTCGTGAGAG			M.marinum

- - - -

	1290	1300	1310	1320	
1264	CGAATCCTTTTAAAGCCGGACTCAGTTCGGATT	GGGGTCT			M.avium
1216	CGAATCCTTTTAAAGCCGGTCTCAGTTCGGATTGGGGTCT				M.intracellulare
1258	CGAATCCTTTTAAAGCCGGACTCAGTTCGGATTGGGGTCT				M.paratuberc.
1224	CGAATCCTTTTAAAGCCGGTCTCAGTTCGGATTGGGGTCT				M.scrofulaceum
1229	CGAATCCTTTAAAGCCGGTCTCAGTTCGGATCGGGGTCT				M.tuberculosis
1368	CGAATCCTTTAAAGCCGGTCTCAGTTCGGATCGGGGTCT				M.bovis
1279	CGAATCCTTTTAAAGCCGGTCTCAGTTCGGATCGGGGTCT				M.leprae
1226	CGAATCCTTTTAAAGCCGGTCTCAGTTCGGATCGGGGTCT				M.kansasii
1227	CGAATCCTTTTAAAGCCGGTCTCAGTTCGGATCGGGGTCT				M.gastri
1260	CGAATCCTTTTAAAGCCGGTCTCAGTTCGGATCGGGGTCT				M.gordonae
1221	CGAATCCTTTAAAGCCGGTCTCAGTTCGGATCGGGGTCT				M.marinum

	1330	1340	1350	1360	
1304	GCAACTCGACCCCATGAAGTCGGAGTCGCTAGTAATCGCA				M.avium
1256	GCAACTCGACCCCATGAAGTCGGAGTCGCTAGTAATCGCA				M.intracellulare
1298	GCAACTAGACCCCATGAAGTCGGAGTCGCTAGTAATCGCA				M.paratuberc.
1264	GCAACTCGACCCCATGAAGTCGGAGTCGCTAGTAATCGCA				M.scrofulaceum
1268	GCAACTCGACCCCATGAAGTCGGAGTCGCTAGTAATCGCA				M.tuberculosis
1407	GCAACTCGACCCCATGAAGTCGGAGTCGCTAGTAATCGCA				M.bovis
1319	GCAACTCGACCCCATGAAGTCGGAGTCGCTAGTAATCGCA				M.leprae
1266	GCAACTCGACCCCATGAAGTCGGAGTCGCTAGTAATCGCA				M.kansasii
1267	GCAACTCGACCCCATGAAGTCGGAGTCGCTAGTAATCGCA				M.gastri
1300	GCAACTCGACCCCATGAAGTCGGAGTCGCTAGTAATCGCA				M.gordonae
1260	GCAACTCGACCCCATGAAGTCGGAGTCGCTAGTAATCGCA				M.marinum

Figure 5B

25500T 224680

30/31

2550 | TTACGCGGCGGACGACGAAAGACCCCGGACCTTCACTA 2589 |
2568 2569 |

Mavium 23S:

Figure 6

441 | TGGAGAGAAGCACC GGCCA ACTACGTGCCAGCAGCGCGGTAAATACGTAG 491
452 |
473 474 477 |
843 | GTACGGCCGCAAGGCTAAAACTC AAGGAATTGACGGGGGC 883
865 866 |

Figure 7